Page 8, first full paragraph:

A multitude of sequences is known which code for membrane proteins of unknown function. By providing in accordance with the invention export genes such as the export gene with the nucleotide sequence of nucleotide 1016 to 1726 in accordance with SEQ ID No. 1 and table 2 or respectively, the corresponding export proteins for example that with the amino acid sequence according to SEQ ID No. 2, it is now possible to identify by sequence comparison membrane proteins, whose function is the transport of amino acids. The export gene identified in this way can subsequently be used to improve the amino acid production in accordance with the process of the invention.

Page 8, second full paragraph:

The membrane proteins known from the state-of-the-art generally include 12, some also only 4 transmembrane helices. However, it has now been found surprisingly that the membrane proteins responsible or suitable for the export of amino acids include 6 transmembrane helices (see for example, the amino acid sequence of an export protein listed in SEQ ID No. 2 and table 3, wherein the 6 transmembrane areas have been highlighted by underlining). Consequently, there is a new class of membrane proteins present, which has not yet been described.

Page 11/12 bridging paragraph:

The nucleotide sequence of the 2.3kb BamH1 fragment was performed according to the dideoxy-chain termination method of Sanger et al. (Proc. Natl. Acad. Sci USA(1977) 74:5463-5467) and the sequencing reaction with the Auto Read Sequencing kit from Pharamcia (Uppsala, Sweden). The electrophoretic analysis occurs with the automatic laser-fluorescence DNA sequenc-

ing apparatus (A.L.F) from Pharmacia-LKB(Piscataway, NJ, USA). The nucleotide sequence obtained was analyzed by the program packet HUSAR (Release 3.0) of the German Cancer Research Center (Heidelberg). The nucleotide sequence and the result of the analysis is presented in SEQ ID No [(A)]1 and Fig. 2. The analysis results in two fully open reading frames (ORF) on the sequenced DNA piece. ORF1 codes for a protein with a length of 236 amino acids, OFR2 codes for a protein with a length of 290 amino acids. The protein derived from ORF1 includes an accumulation of hydrophobic amino acids as they are characteristic for membrane-embedded proteins. The detailed analysis of the distribution of the hydrophobic and hydrophilic amino acids by the programs PHD.HTM (Protein Science(1995)4:521-533) is shown in table 3. It is apparent therefrom that the protein contains six hydrophobic helix areas which extend through the membrane. Consequently, this protein is the searched for exporter of the amino acid L-lysine. The corresponding gene will therefore be designated below as lysE. In table 2, it is marked accordingly. ORF2 is transcribed in a direction opposite to ORF1. The sequence analysis shows that ORF2 has a high identity with regulator genes which are combined as a single family (Ann Rev Microbiol(1993) 597-626). Genes of this family regulate the expression processes of the various genes involved in catabolic or anabolic processes in a positive way. For this reason, ORF2 will below be designated as lysG (Govern=regulating). Because of the coordination and because lysE could be cloned (see a)) and subcloned (see b)) together with lysG, lysG is regulator of lysE and consequently also participates in the lysine export. The gene lysG and the amino acid sequence derived therefrom are also shown in SEQ ID No(B)1 and table 2 and, respectively, SEQ ID No.3.

Page 15, Sequence Protocol A:

Sequence protocol A:

SEQ ID No. 1: Nucleotide sequence of the coding DNA strand and the amino acid sequence of the Lysine-exporter LysE derived therefrom.

SEQ ID No. 2: Amino acid sequence of the Lysine-exporter LysE.

Sequence Protocol B:

SEQ ID No.(B)1: Nucleotide sequence of the anti-sense strand and
Amino acid sequences of the Lysine-exporter-regulator $LysG_1$ derived therefrom and a ORF3.

SEQ ID No.(B)2: Amino acid sequence of the open reading frame (partial) ORF3.

SEQ ID No. 3: Amino acid sequence of the Lysine exporter-Regulator $LysG_1$..

Page 16, cancel Table 1.

Pages 17 -19, cancel Table 2.

Page 20, cancel Table 3.

Please amend the claims as follows:

1. A process for the microbacterial production of amino acids, comprising the steps of: providing a microbial organism having a certain export carrier activity and a certain export gene-expression,

increasing, selectively, one of